

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Bartley, Timothy D.
Bogenberger, Jakob M.
Rosselman, Robert A.
Hunt, Pamela
Kinstler, Olaf B.
Samal, Babru B.

(ii) TITLE OF INVENTION: Compositions and Methods for Stimulating
Megakaryocyte Growth and Differentiation

(iii) NUMBER OF SEQUENCES: 34

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Amgen Inc.
(B) STREET: 1840 Dehavilland Drive
(C) CITY: Thousand Oaks
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 91320-1789

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Cook, Robert R.
(C) REFERENCE/DOCKET NUMBER: A-290-C

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Met Leu Arg Asp
1 5 10 15

Ser His Val Leu His Xaa Arg Leu Xaa Gln Xaa Pro Asp Ile Tyr
20 25 30

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Met Leu Arg Asp
1 5 10 15

Ser His Val Leu His
20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Thr Gln Lys Glu Gln Thr Lys Ala Gln Asp Val Leu Gly Ala Val Ala
1 5 10 15

Leu

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCNCCNCCNG CNTGYGA

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCARTGYAAC ACRTGNGART C

21

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp
1 5 10 15
Ser His Val Leu His
 20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTACGCGTTC TAGANNNNNN T

21

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGTTTACTGA GGACTCGGAG G

21

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCGGCCGGA TAGGCCTTTT TTTTTTTTTT

30

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTCGGCCGGA TAGGCCTTTT TTTTTTTTTT

29

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCGACCTCC GAGTCCTCAG

20

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAGTCCTCAG TAAACTGCTT CGT

23

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGAGTCACGA AGCAGTTTAC

20

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCTTTACTTC TAGGCCTG

18

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAGGTCACAA GCAGGAGGA

19

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGCATAGTCC GGGACGTCG

19

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TCCTCCTGCT TGTGACCTC

19

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAGGAAGGA TTCAGGGGA

19

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAACAAGTCG ACCGCCAGCC AGACACCCCG

30

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCCGGATAG GCCACTCNNN NNNT

24

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCARTGYAAN ACRTGNGART C

21

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTGGTGTGCA CTTGTG

16

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CACAAGTGCA CACCAACCCC

20

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1342 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 99..1094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CAGGGAGCCA CGCCAGCCAA GACACCCCGG CCAGATGGA GCTGACTGAA TTGCTCCTCG

60

TGGTCATGCT TCTCCTAACT GCAAGGCTAA CGCTGTCC AGC CCG GCT CCT CCT
 Ser Pro Ala Pro Pro
 1 5

113

GCT TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT GAC TCC CAT GTC 161
 Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val
 10 15 20
 CTT CAC AGC AGA CTG AGC CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA 209
 Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr
 25 30 35
 CCT GTC CTG CTG CCT GCT GTG GAC TTT AGC TTG GGA GAA TGG AAA ACC 257
 Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr
 40 45 50
 CAG ATG GAG GAG ACC AAG GCA CAG GAC ATT CTG GGA GCA GTG ACC CTT 305
 Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
 55 60 65
 CTG CTG GAG GGA GTG ATG GCA GCA CGG GGA CAA CTG GGA CCC ACT TGC 353
 Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys
 70 75 80 85
 CTC TCA TCC CTC CTG GGG CAG CTT TCT GGA CAG GTC CGT CTC CTC CTT 401
 Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu
 90 95 100
 GGG GCC CTG CAG AGC CTC CTT GGA ACC CAG CTT CCT CCA CAG GGC AGG 449
 Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg
 105 110 115
 ACC ACA GCT CAC AAG GAT CCC AAT GCC ATC TTC CTG AGC TTC CAA CAC 497
 Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His
 120 125 130
 CTG CTC CGA GGA AAG GTG CGT TTC CTG ATG CTT GTA GGA GGG TCC ACC 545
 Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu Val Gly Gly Ser Thr
 135 140 145
 CTC TGC GTC AGG CGG GCC CCA CCC ACC ACA GCT GTC CCC AGC AGA ACC 593
 Leu Cys Val Arg Arg Ala Pro Pro Thr Thr Ala Val Pro Ser Arg Thr
 150 155 160 165
 TCT CTA GTC CTC ACA CTG AAC GAG CTC CCA AAC AGG ACT TCT GGA TTG 641
 Ser Leu Val Leu Thr Leu Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu
 170 175 180
 TTG GAG ACA AAC TTC ACT GCC TCA GCC AGA ACT ACT GGC TCT GGG CTT 689
 Leu Glu Thr Asn Phe Thr Ala Ser Ala Arg Thr Thr Gly Ser Gly Leu
 185 190 195
 CTG AAG TGG CAG CAG GGA TTC AGA GCC AAG ATT CCT GGT CTG CTG AAC 737
 Leu Lys Trp Gln Gln Gly Phe Arg Ala Lys Ile Pro Gly Leu Leu Asn
 200 205 210
 CAA ACC TCC AGG TCC CTG GAC CAA ATC CCC GGA TAC CTG AAC AGG ATA 785
 Gln Thr Ser Arg Ser Leu Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile
 215 220 225

CAC GAA CTC TTG AAT GGA ACT CGT GGA CTC TTT CCT GGA CCC TCA CGC 833
His Gln Leu Leu Asn Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg
230 235 240 245
AGG ACC GTA GGA GCC CCG GAC ATT TCC TCA GGA ACA TCA GAC ACA GGC 881
Arg Thr Leu Gly Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly
250 255 260
TCC CTG CCA CCC AAC CTC CAG CCT GGA TAT TCT CCT TCC CCA ACC CAT 929
Ser Leu Pro Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His
265 270 275
CCT CCT ACT GGA CAG TAT ACG CTC TTC CCT CTT CCA CCC ACC TTG CCC 977
Pro Pro Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro
280 285 290
ACC CCT GTG GTC CAG CTC CAC CCC CTG CTT CCT GAC CCT TCT GCT CCA 1025
Thr Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro
295 300 305
ACG CCC ACC CCT ACC AGC CCT CTT CTA AAC ACA TCC TAC ACC CAC TCC 1073
Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His Ser
310 315 320 325
CAG AAT CTG TCT CAG GAA GGG TAAGCTTCTC AGACACTGCC GACATCAGCA 1124
Gln Asn Leu Ser Gln Glu Gly
330
TTGTCTCGTG TACAGCTCCC TTCCCTGCAG GGCGCCCTG GGAGACAACT GGACAAGATT 1184
TCCTACTTTC TCCTGAAACC CAAAGCCCTG GTAAAAGGGA TACACAGGAC TGAAAAGGGA 1244
ATCATTTTTC ACTGTACATT ATAAACCTTC AGAAGCTATT TTTTAAAGCT ATCAGCAATA 1304
CTCATCAGAG CAGCTAGCTC TTTGGTCTAT TTTCTGCA 1342

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu
1 5 10 15
Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val
20 25 30
His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu
35 40 45

Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu
 50 55 60
 Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln
 65 70 75 80
 Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln
 85 90 95
 Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu
 100 105 110
 Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe
 115 120 125
 Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
 130 135 140
 Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr Ala
 145 150 155 160
 Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu Pro Asn
 165 170 175
 Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser Ala Arg Thr
 180 185 190
 Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe Arg Ala Lys Ile
 195 200 205
 Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu Asp Gln Ile Pro Gly
 210 215 220
 Tyr Leu Asn Arg Ile His Glu Leu Leu Asn Gly Thr Arg Gly Leu Phe
 225 230 235 240
 Pro Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro Asp Ile Ser Ser Gly
 245 250 255
 Thr Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu Gln Pro Gly Tyr Ser
 260 265 270
 Pro Ser Pro Thr His Pro Pro Thr Gly Gln Tyr Thr Leu Phe Pro Leu
 275 280 285
 Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu His Pro Leu Leu Pro
 290 295 300
 Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr
 305 310 315 320
 Ser Tyr Thr His Ser Gln Asn Leu Ser Gln Glu Gly
 325 330

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 99..621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CAGGGAGCCA CGCCAGCCAA GACACCCGG CCAGAATGGA GCTGACTGAA TTGCTCCTCG 60

TGGTCATGCT TCTCCTAACT GCAAGGCTAA CGCTGTCC AGC CCG GCT CCT CCT 113
 Ser Pro Ala Pro Pro
 1 5

GCT TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT GAC TCC CAT GTC 161
 Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val
 10 15 20

CTT CAC AGC AGA CTG AGC CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA 209
 Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr
 25 30 35

CCT GTC CTG CTG CCT GCT GTG GAC TTT AGC TTG GGA GAA TGG AAA ACC 257
 Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr
 40 45 50

CAG ATG GAG GAG ACC AAG GCA CAG GAC ATT CTG GGA CCA GTG ACC CTT 305
 Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
 55 60 65

CTG CTG GAG GGA GTG ATG GCA GCA CGG GGA CAA CTG GGA CCC ACT TGC 353
 Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys
 70 75 80 85

CTC TCA TCC CTC CTG GGG CAG CTT TCT GGA CAG GTC CGT CTC CTC CTT 401
 Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu
 90 95 100

GGG GCC CTG CAG AGC CTC CTT GGA ACC CAG CTT CCT CCA CAG GGC AGG 449
 Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg
 105 110 115

ACC ACA GCT CAC AAG GAT CCC AAT GCC ATC TTC CTG AGC TTC CAA CAC 497
 Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His
 120 125 130

TG CTC CGA GGA AAG GTG CGT TTC CTG ATG CTT GTA GGA GGG TCC ACC 545
 Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu Val Gly Gly Ser Thr
 135 140 145
 CTC TGC GTC AGG CGG GCC CCA CCC ACC ACA GCT GTC CCC AGC AGA ACC 593
 Leu Cys Val Arg Arg Ala Pro Pro Thr Thr Ala Val Pro Ser Arg Thr
 150 155 160 165
 TCT CTA GTC CTC ACA CTG AAC GAG CTC C CAAACAGGAC TTCTGGATTG 641
 Ser Leu Val Leu Thr Leu Asn Glu Leu
 170
 TTGGAGACAA ACTTCACTGC CTCAGCCAGA ACTACTGGCT CTGGGCTTCT GAAGTGGCAG 701
 CAGGGATTCA GAGCCAAGAT TCCTGGTCTG CTGAACCAAA CCTCCAGGTC CCTGGACCAA 761
 ATCCCCGGAT ACCTGAACAG GATACACGAA CTCTTGAATG GAACTCGTGG ACTCTTTCCT 821
 GGACCCTCAC GCAGGACCCT AGGAGCCCCG GACATTTTCT CAGGAACATC AGACACAGGC 881
 TCCCTGCCAC CCAACCTCCA GCCTGCATAT TCTCCTTCCC CAACCCATCC TCCTACTGGA 941
 CAGTATACGC TCTTCCCTCT TCCACCCACC TTGCCCACCC CTGTGGTCCA GCTCCACCCC 1001
 CTGCTTCCTG ACCCTTCTGC TCCAACGCCC ACCCCTACCA GCCCTCTTCT AAACACATCC 1061
 TACACCCACT CCCAGAATCT GTCTCAGGAA GGGTAAGGT CTCAGACACT GCCGACATCA 1121
 GCATTGTCTC GTGTACAGCT CCCTTCCCTG CAGGCGCCCC CTGGGAGACA ACTGGACAAG 1181
 ATTCCTACT TTCTCCTGAA ACCCAAAGCC CTGGTAAAG GGATACACAG GACTGAAAAG 1241
 GGAATCATTT TTTACTGTAC ATTATAAACC TTCAGAAGCT ATTTTTTTTAA GCTATCAGCA 1301
 ATACTCATCA GAGCAGCTAG CTCTTTGGTC TATTTTCTGC A 1342

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu
 1 5 10 15
 Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val
 20 25 30
 His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu
 35 40 45

Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu
50 55 60

Gly Ala Val Thr Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln
65 70 75 80

Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln
85 90 95

Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu
100 105 110

Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe
115 120 125

Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
130 135 140

Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr Ala
145 150 155 160

Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu
165 170

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 97..894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGGAGCCAC GCCAGCCAGA CACCCCGGCC AGAATGGAGC TGACTGAATT GCTCCTCGTG 60

GTCATGCTTC TCCTAACTGC AAGGCTAACG CTGTCC AGC CCG GCT CCT CCT GCT 114
Ser Pro Ala Pro Pro Ala
1 5

TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT GAC TCC CAT GTC CTT 162
Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu
10 15 20

CAC AGC AGA CTG AGC CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA CCT 210
His Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro
25 30 35

GTC	CTG	CTG	CCT	GCT	GTG	GAC	TTT	AGC	TTG	GGA	GAA	TGG	AAA	ACC	CAG	258
Val	Leu	Leu	Pro	Ala	Val	Asp	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	
40						45					50					
ATG	GAG	GAG	ACC	AAG	GCA	CAG	GAC	ATT	CTG	GGA	GCA	GTG	ACC	CTT	CTG	306
Met	Glu	Glu	Thr	Lys	Ala	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	
55					60					65					70	
CTG	GAG	GGA	GTG	ATG	GCA	GCA	CGG	GGA	CAA	CTG	GGA	CCC	ACT	TGC	CTC	354
Leu	Glu	Gly	Val	Met	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	
				75					80					85		
TCA	TCC	CTC	CTG	GGG	CAG	CTT	TCT	GGA	CAG	GTC	CGT	CTC	CTC	CTT	GGG	402
Ser	Ser	Leu	Leu	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	
			90					95					100			
GCC	CTG	CAG	AGC	CTC	CTT	GGA	ACC	CAG	CTT	CCT	CCA	CAG	GGC	AGG	ACC	450
Ala	Leu	Gln	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	
		105					110					115				
ACA	GCT	CAC	AAG	GAT	CCC	AAT	GCC	ATC	TTC	CTG	AGC	TTC	CAA	CAC	CTG	498
Thr	Ala	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	
	120					125					130					
CTC	CGA	GGA	AAG	GAC	TTC	TGG	ATT	GTT	GGA	GAC	AAA	CTT	CAC	TGC	CTC	546
Leu	Arg	Gly	Lys	Asp	Phe	Trp	Ile	Val	Gly	Asp	Lys	Leu	His	Cys	Leu	
135					140				145					150		
AGC	CAG	AAC	TAC	TGG	CTC	TGG	GCT	TCT	GAA	GTG	GCA	GCA	GGG	ATT	CAG	594
Ser	Gln	Asn	Tyr	Trp	Leu	Trp	Ala	Ser	Glu	Val	Ala	Ala	Gly	Ile	Gln	
			155						160					165		
AGC	CAA	GAT	TCC	TGG	TCT	GCT	GAA	CCA	AAC	CTC	CAG	GTC	CCT	GGA	CCA	642
Ser	Gln	Asp	Ser	Trp	Ser	Ala	Glu	Pro	Asn	Leu	Gln	Val	Pro	Gly	Pro	
			170					175					180			
AAT	CCC	CGG	ATA	CCT	GAA	CAG	GAT	ACA	CGA	ACT	CTT	GAA	TGG	AAC	TCG	690
Asn	Pro	Arg	Ile	Pro	Glu	Gln	Asp	Thr	Arg	Thr	Leu	Glu	Trp	Asn	Ser	
		185					190					195				
TGG	ACT	CTT	TCC	TGG	ACC	CTC	ACG	CAG	GAC	CCT	AGG	AGC	CCC	GGA	CAT	738
Trp	Thr	Leu	Ser	Trp	Thr	Leu	Thr	Gln	Asp	Pro	Arg	Ser	Pro	Gly	His	
	200					205					210					
TTC	CTC	AGG	AAC	ATC	AGA	CAC	AGG	CTC	CCT	GCC	ACC	CAA	CCT	CCA	GCC	786
Phe	Leu	Arg	Asn	Ile	Arg	His	Arg	Leu	Pro	Ala	Thr	Gln	Pro	Pro	Ala	
215					220					225					230	
TGG	ATA	TTC	TCC	TTC	CCC	AAC	CCA	TCC	TCC	TAC	TGG	ACA	GTA	TAC	GCT	834
Trp	Ile	Phe	Ser	Phe	Pro	Asn	Pro	Ser	Ser	Tyr	Trp	Thr	Val	Tyr	Ala	
				235					240					245		
CTT	CCC	TCT	TCC	ACC	CAC	CTT	GCC	CAC	CCC	TGT	GGT	CCA	GCT	CCA	CCC	882
Leu	Pro	Ser	Ser	Thr	His	Leu	Ala	His	Pro	Cys	Gly	Pro	Ala	Pro	Pro	
			250					255					260			

CCT GCT TCC TGACCCTTCT GCTCCAACGC CCACCCCTAC CAGCCCTCTT 931
 Pro Ala Ser
 265

CTAAACACAT CCTACACCOA CTCCCAGAAT CTGTCTCAGG AAGGGTAAGG TTCTCAGACA 991
 CTGCCGACAT CAGCATTGTC TCGTGTACAG CTCCCTTCCC TGCAGGGCGC CCCTGGGAGA 1051
 CAACTGGACA AGATTTCTTA CTTTCTCCTG AAACCCAAAG CCCTGGTAAA AGGGATACAC 1111
 AGGACTGAAA AGGGAATCAT TTTTCACTGT ACATTATAAA CCTTCAGAAG CTA 1164

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu
 1 5 10 15

Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val
 20 25 30

His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu
 35 40 45

Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu
 50 55 60

Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln
 65 70 75 80

Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln
 85 90 95

Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu
 100 105 110

Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe
 115 120 125

Leu Ser Phe Gln His Leu Leu Arg Gly Lys Asp Phe Trp Ile Val Gly
 130 135 140

Asp Lys Leu His Cys Leu Ser Gln Asn Tyr Trp Leu Trp Ala Ser Glu
 145 150 155 160

Val Ala Ala Gly Ile Gln Ser Gln Asp Ser Trp Ser Ala Glu Pro Asn
 165 170 175

Leu Gln Val Pro Gly Pro Asn Pro Arg Ile Pro Glu Gln Asp Thr Arg
180 185 190

Thr Leu Glu Trp Asn Ser Trp Thr Leu Ser Trp Thr Leu Thr Gln Asp
195 200 205

Pro Arg Ser Pro Gly His Phe Leu Arg Asn Ile Arg His Arg Leu Pro
210 215 220

Ala Thr Gln Pro Pro Ala Trp Ile Phe Ser Phe Pro Asn Pro Ser Ser
225 230 235 240

Tyr Trp Thr Val Tyr Ala Leu Pro Ser Ser Thr His Leu Ala His Pro
245 250 255

Cys Gly Pro Ala Pro Pro Pro Ala Ser
260 265

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAGCTCACTA GTGTCGACCT GCAG

24

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTGCAGGTCG AACTAGTGA GCTC

24

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTCATAATTT TTAAAAAATT CATTGACAA ATGCTAAAT TCTTGATTAA TATTCTCAAT 60
TGTGAGCGCT CACAATTTAT 80

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGATAAATTG TGAGCGCTCA CAATTGAGAA TATTAATCAA GAATTTTAGC ATTTGTCAAA 60
TGAATTTTTT AAAAATTATG AGACGT 86

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GACGTCTCAT AATTTTTTAAA AAATTCATT GACAAATGCT AAAATTCTTG ATTAATATTC 60
TCAATTGTGA GCGCTCACAA TTTATCGAT 89